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OZ.5366

PRELIMINARY; PRT; 476 AA.

AC O25366;
DT 01-JAN-1998 (TREMELrel. 05, Last sequence update)
DT 01-JAN-1998 (TREMELrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE 01-MAR-2004 (TREMELrel. 26, Last annotation update)
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GO; GO:0016757; F:transferase activity, transferring glycosyl. ..;
Complete proteome; Glycosyltransferase; Transferase.
SEQUENCE 476 AA; 55926 MW; 32BFFDBBD36E1F74 CRC64;
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Matches 376
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MEDLINE=97394467; PubMed=9252185; DOI=10.1038/41483;

Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.

Pleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S.R.,

Pleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S.R.,

Dougherty B.A., Nelson K.B., Quackenbush J., Zhou L., Kirkness Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.J., Khala Glodek A., McKenney K., PitzGerald L.M., Lee N., Adams M.D.,

Hickey B.K., Berg D.B., Gocayne J.D., Utterback T.R., Peterson Kelley J.M., Cotton M.D., Weidman J.F., Pujii C., Bowman C.,

Watthey L., Wallin B., Hayes W.S., Borodovsky M., Karp P.D.,

Smith H.O., Fraser C.M., Venter J.C.;
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025142;
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STRAIN=26695 /
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
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01-JAN-1998 (TrEMBLrel. 05,
01-MAR-2004 (TrEMBLrel. 26,
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01-JAN-1998
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                               HPNAYLDMLYENPLNALDGKAYFYQDLSFKKILAFFKTILENDTIYHKSSTSFMMBCDLD
                                                                                                                                           NSQGYGYYTEKILDAYFSHTIPIYWGSPSVAKDFNPKEFVNVHDFNNFDEAIDYIKYLHT
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Pred. No. 3.7e-124;
9; Mismatches 24;
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Q9ZLI3;
01-MAY-1999
01-MAY-1999
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SEQUENCE FROM N.A.

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SEQUENCE FROM N.A.

MEDLINE=99120557; PubMed=9923682; DOI=10.1038/16495;

MEDLINE=99120557; PubMed=9923682; DOI=10.1038/16495;

Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown B.D., Doi, Smith D.R., Noonan B., Guild B.C.; deJonge B.L., Carmel G., Smith D.R., Noonan B., Guild B.C.; deJonge B.L., Carmel G., Tummino P.J., Caruso A., Uria-Nickelben M., Mills D.M., Ives Tummino P.J., Caruso A., Uria-Nickelben M., Mills D.M., Taylor D.E., Vov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genomic sequence comparison of two unrelated isolates of the legastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
RMBL; AE001491; AAD06169.1; -
RMBL; B71914; B71914.
G0; G0:0016757; F:transferase activity, transferring glycosyl.
Complete proteome; Glycosyltransferase; Transferase.
SEQUENCE 454 AA; 53448 MW; 3262687131263ABO CRC64;
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Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
ALPHA (1,3)-FUCOSYLTRANSFERASE.
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QNASPLLELSQNTSFKIYRKAYQKPI
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Pred. No. 3e-1
25; Mismatches
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Best Local &
Matches 365
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MEDLINE-99120557; PubMed=9923682; DOI=10.1038/16495;
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown B.D.,
Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.
Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Iv
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.B.,
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gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
EMBL; AERO01528; AAD06573.1; -
PIR; G71862; G71862.
G0; G0:0016757; F:transferase activity, transferring glycosyl.
Complete proteome; Glycosyltransferase; Transferase.
SEQUENCE 436 AA; 50698 MW; 1DB2066AE98FA61E CRC64;
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ALPHA-(1,3)-FUCOSYLTRANSFERASE.
OrderedLocusNames=JHP1002;
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Bacteria; Proteobacteria; Epsilonproteobacteria; Ca
Helicobacteraceae; Helicobacter.
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BLSQNTTFKIYRKAYQKSL
                                 ELSONTSFKIYRKAYOKPI
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Pred. No. 2e-120;
0; Mismatches 34;
    421
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annotation update)
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RBSULT 6 Q6ST35 ID Q6ST35

PRELIMINARY;

PRT;

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ALIGNMENTS

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RESULT 1
US-10-120-319-1
; Sequence 1, Application US/10120319
; Publication No. US20020164749A1
; Publication No. US20020164749A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane B.
APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANFERASE
; FILE REFERENCE: 07254/049001
; CURRENT APPLICATION NUMBER: US/10/120,319
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: 09/092,315
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-05
; PRIOR PILING DATE: EARLIER FILING DATE: 1998-06-05
; PRIOR PILING DATE: EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PASTSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-120-319-1

Query Match 87.4%; Score 2086; DB 13; Length 464;
Best Local Similarity 87.4%; Pred. No. 1.2e-165;
DATE OF A STATE O
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Tue May 24 08:36:55 2005

pct-us05-01614

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   407 YERLLQNASPLLELSQNTSFKIYRKAYQKPI 437
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419 YERLLSKATPLLELSQNTTSKIYRKAYQKSL 449
Qy
Db
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- RESULT 2
 US-10-189-977-1
 ; Sequence 1, Application US/10189977
 ; Publication No. US20030166211A1
 ; GENERAL INFORMATION:

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GENERAL INFORMATION:

APPLICANT: The Governers of the University of Alberta, a Canada Corporation

APPLICANT: Taylor, Diane B.

APPLICANT: Ge, Zhongming

FITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3

FITLE OF INVENTION: EXPRESSING THEM

FITLE OF INVENTION: EXPRESSING THEM

FILLS OF INVENTION UNUMBER: US/09/733,524

CURRENT APPLICATION NUMBER: US/09/733,524

CURRENT APPLICATION NUMBER: 09/092,315

PRIOR APPLICATION NUMBER: 09/092,315

PRIOR FILING DATE: 1998-06-05

PRIOR FILING DATE: 1998-06-05

PRIOR FILING DATE: 1997-06-06

NUMBER OF SEQ ID NOS: 20

SOFTWARE: FastSEQ for Windows Version 4.0
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US-09-733-524-1
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                                                      Query Match
Best Local Sim
Matches 393;
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09733524
Patent No. US20020068347A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 393; Conserv
                                                                                                                                                                        SEQ ID NO 1
                                                                                                                         LENGTH: 501
TYPE: PRT
ORGANISM: Helicobacter pylori fucosyltransferase
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                                                                     Similarity
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 MFQPLLDAYVESASIEKWASKSPPPLKIAVANWWGDEEIKEFKNSVLYFILSQRYTITLH
                  MPQPLLDAYVESASIEKMASKSPPPLKIAVANWWGDEEIKEFKKSVLYFIFSQRYTIALH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YDDLRVNYDDLRVNYERLLSKATPLLELSQNTTSKIYRKAYQKSL 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YDDIRVNYDDIRVNYBRILQNASPILBISQNTSFKIYRKAYQKPI 437
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84.5%; Pred. No. 1.5e-164;
tive 15; Mismatches 27;
                                                     86.8%; Score 2073; DB 9;
87.1%; Pred. No. 1.6e-164;
tive 15; Mismatches 27;
                                                                                 Length
                                                        Indels
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US-10-120-319-8
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Best Local S
Matches 384
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SQGYGYVTEKILDAYFSHTIPIYWGSPSVAKOFNPKBFVNVHDFNNPDBAIDYIKYLHTH
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                                                                                                                    PLASIDDLRV--------YYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVN
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                                                                                     PLYTIDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRINYDDLRVNYDDLRVN
449
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Sequence 8, Application US/10120319

Publication No. US20020164749A1

GENERAL INFORMATION:
APPLICANT: Taylor, Diane B.
APPLICANT: Ge, Zhongming
ITITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANFERASE
FILE REFERENCE: 07254/049001

CURRENT FILING DATE: 2002-04-09

PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: 09/092,315

PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-05

PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: US 60/048,857

PRIOR FILING DATE: EARLIER FILING DATE: 1997-06-06 NUMBER OF SEQ ID NOS: 22

SOPTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 8

LENGTH: 454

TYPE: PRT
ORGANISM: Helicobacter pylori US 60/048,857

1 MFQPLLDAYVESASIEKWASKSPPPLKIAVANWWGDEEIKEFKKSVLYFIFSQRYTIALH GVVSFVASNANAPMENAFYDALNSIEPVTGGGSVKNTLGYNVKNKSEFLSQYKFNLCFEN 240 RMPLYYDRLHHKARSVNDTTSPYKLKDNSLYTLKKPSHQFKENHPNLCAVVNDESDPLKR RNPDKPADIVFGNPLGSARKILSYQNTKRIFYTGENESPNFNLFDYAIGFDELDFRDRYL QNPNEFSDLVFSNPLGSARKILSYQNAKRVFYTGENEVPNFNLFDYAIGFDELDFRDRYL |||:::|| MFQPLLDAFIESASIEKMASKSPPPLKIAVANWWGDEEIKGFKKSTLYFILSQHYTITLH GFAS FVASNANAPMRNAFYDALNS I EPVTGGGAVKNTLGYKVGNKSEFLSQYKFNLCFEN RMPLYYDRLHHKABSVNDTTAPYKI KGNSLYTLKKPSHCFKENHPNLCALINNESDPLKR Conservative 27; Mismatches 9; Gaps . 180 120 240 180 120 60 2